

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: He, Wei-Wu et al.
- (ii) TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme
Like Apoptosis Protease 3 and 4
- (iii) NUMBER OF SEQUENCES: 12
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Human Genome Sciences, Inc.
(B) STREET: 9410 Key West Ave.
(C) CITY: Rockville
(D) STATE: MD
(E) COUNTRY: USA
(F) ZIP: 20850
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/462,969
(B) FILING DATE: 05-JUN-1995
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/334,251
(B) FILING DATE: 11-NOV-1994
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Brookes, A. Anders
(B) REGISTRATION NUMBER: 36,373
(C) REFERENCE/DOCKET NUMBER: PF140P1
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 301-309-8504
(B) TELEFAX: 301-309-8439

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1371 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCACGAGAAA CTTTGCTGTG CGCGTTCTCC CGCGCGCGGG CTCAACTTTG TAGAGCGAGG

60

GGCCAACTTG	GCAGAGCGCG	CGGCCAGCTT	TGCAGAGAGC	GCCCTCCAGG	GA	CTATGCGT	120
GCGGGGACAC	GGGTCGCTTT	GGGCTCTTCC	ACCCCTGCGG	AGCGCACTAC	CCC	GAGCCAG	180
GGGCGGTGCA	AGCCCCGCCC	GGCCCTACCC	AGGGCGGCTC	CTCCCTCCGC	AGCGCCGAGA		240
CTTTTAGTTT	CGCTTTCGCT	AAAGGGGCCC	CAGACCCTTG	CTGCGGAGCG	ACGGAGAGAG		300
ACTGTGCCAG	TCCCAGCCGC	CCTACCGCCG	TGGGAACGAT	GGCAGATGAT	TCAGGGCTGT		360
ATTGAAGAGC	AGGGGGTTGA	GGATTTCAGCA	AATGAAGATT	CAGTGGATGC	TAAGCCAGAC		420
CGGTCCCTCGT	TTGTACCGTC	CCTCTTCAGT	AAGAAGAAGA	AAAATGTCAC	CATGCGATCC		480
ATCAAGACCA	CCCGGGACCG	AGTGCCTACA	TATCAGTACA	ACATGAATTT	TGAAAAGCTG		540
GGCAAATGCA	TCATAATAAA	CAACAAGAAC	TTTGATAAAG	TGACAGGTAT	GGGCGTTCGA		600
AACGGAACAG	ACAAAGATGC	CGAGGCGCTC	TTCAAGTGCT	TCCGAAGCCT	GGGTTTTGAC		660
GTGATTGTCT	ATAATGACTG	CTCTTG TGCC	AAGATGCAAG	ATCTGCTTAA	AAAAGCTTCT		720
GAAGAGGACC	ATACAAATGC	CGCCTGCTTC	GCCTGCATCC	TCTTAAGCCA	TGGAGAAGAA		780
AATGTAATTT	ATGGGAAAGA	TGGTGT CACA	CCAATAAAGG	ATTTGACAGC	CCACTTTAGG		840
GGGGATAGAT	GCAAAACCCT	TTTAGAGAAA	CCCAA	ACTCT	TCTTCATTCA	GGCTTGCCGA	900
GGGACCGAGC	TTGATGATGG	CATCCAGGCC	GACTCGGGGC	CCATCAATGA	CACAGATGCT		960
AATCCTCGAT	ACAAGATCCC	AGTGGAAGCT	GACTTCCTCT	TCGCCTATTC	CACGGTTCCA		1020
GGCTATTACT	CGTGGAGGAG	CCCAGGAAGA	GGCTCCTGGT	TTGTGCAAGC	CCTCTGCTCC		1080
ATCCTGGAGG	AGCACGGA	AGACCTGGAA	ATCATGCAAA	TCCTCCACCA	GGGTGAATGA		1140
CAGAGTTGCC	AGGCAC TTTG	AGTCTCAGTC	TGATGACCCA	CACTTCCATG	AGAAGAAGCA		1200
GATCCCCTGT	GTGGTCTCCA	TGCTACCAA	GGA	ACTCTAC	TTCAGTCAAT	AGCCATATCA	1260
GGGGTACATT	CTAGCTGAGA	AGCAATGGGT	CACTCATTA	TGAATCACAT	TTTTTTATGC		1320
TCTTGAAATA	TTCAGAAATT	CTCCAGGATT	TTAATTT	CAG	GAAAATGTAT	T	1371

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Asp Asp Gln Gly Cys Ile Glu Glu Gln Gly Val Glu Asp Ser

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCACGAGCGG ATGGGTGCTA TTGTGAGGCG GTTGTAGAAG AGTTTCGTGA GTGCTCGCAG	60
CTCATACCTG TGGCTGTGTA TCCGTGGCCA CAGCTGGTTG GCGTCGCCTT GAAATCCCAG	120
GCCGTGAGGA GTTAGCGAGC CCTGCTCACA CTCGGCGCTC TGGTTTTTCG TGGGTGTGCC	180
CTGCACCTGC CTCTTCCCGC ATTCTCATT AATAAGGTAT CCATGGAGAA CACTGAAAAC	240
TCAGTGGATT CAAAATCCAT TAAAAATTG GAACCAAAGA TCATACATGG AAGCGAATCA	300
ATGGACTCTG GAATATCCCT GGACAACAGT TATAAAATGG ATTATCCTGA GATGGGTTTA	360
TGTATAATAA TTAATAATAA GAATTTTCAT AAAAGCACTG GAATGACATC TCGGTCTGGT	420
ACAGATGTCG ATGCAGCAA CCTCAGGGAA ACATTCAGAA ACTTGAAATA TGAAGTCAGG	480
AATAAAAATG ATCTTACACG TGAAGAAATT GTGGAATTGA TCGGTGATGT TTCTAAAGAA	540
GATCACAGCA AAAGGAGCAG TTTTGTGTTGT GTGCTTCTGA GCCATGGTGA AGAAGGAATA	600
ATTTTGGAA CAAATGGACC TGTTGACCTG AAAAAATAA CAAACTTTTT CAGAGGGGAT	660
CGTTGTAGAA GTCTAACTGG AAAACCCAAA CTTTTCATTA TTCAGGCCTG CCGTGGTACA	720
GAAGTGGACT GTGGCATTGA GACAGACAGT GGTGTTGATG ATGACATGGC GTGTCATAAA	780
ATACCAGTGG AGGCCGACTT CTTGTATGCA TACTCCACAG CACCTGGTTA TTATTCTTGG	840
CGAAATTCAA AGGATGGCTC CTGGTTCATC CAGTCGCTTT GTGCCATGCT GAAACAGTAT	900
GCCGACAAGC TTGAATTTAT GCACATTCTT ACCCGGGTTA ACCGAAAGGT GGCAACAGAA	960
TTTGAGTCCT TTTCTTTTGA CGCTACTTTT CATGCAAAGA AACAGATTCC ATGTATTGTT	1020
TCCATGCTCA CAAAAGAACT CTATTTTTAT CACTAAAGAA ATGGTTGGTT GGTGGTTTTT	1080
TTTAGTTTGT ATGCCAAGTG AGAAGATGGT ATATTGGGT ACTGTATTTC CCTCTATTG	1140
GGGACCTACT CTCATGCTG	1159

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 277 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Glu Asn Thr Glu Asn Ser Val Asp Ser Lys Ser Ile Lys Asn Leu
1 5 10 15
Glu Pro Lys Ile Ile His Gly Ser Glu Ser Met Asp Ser Gly Ile Ser
20 25 30
Leu Asp Asn Ser Tyr Lys Met Asp Tyr Pro Glu Met Gly Leu Cys Ile
35 40 45
Ile Ile Asn Asn Lys Asn Phe His Lys Ser Thr Gly Met Thr Ser Arg
50 55 60
Ser Gly Thr Asp Val Asp Ala Ala Asn Leu Arg Glu Thr Phe Arg Asn
65 70 75 80
Leu Lys Tyr Glu Val Arg Asn Lys Asn Asp Leu Thr Arg Glu Glu Ile
85 90 95
Val Glu Leu Met Arg Asp Val Ser Lys Glu Asp His Ser Lys Arg Ser
100 105 110
Ser Phe Val Cys Val Leu Leu Ser His Gly Glu Glu Gly Ile Ile Phe
115 120 125
Gly Thr Asn Gly Pro Val Asp Leu Lys Lys Ile Thr Asn Phe Phe Arg
130 135 140
Gly Asp Arg Cys Arg Ser Leu Thr Gly Lys Pro Lys Leu Phe Ile Ile
145 150 155 160
Gln Ala Cys Arg Gly Thr Glu Leu Asp Cys Gly Ile Glu Thr Asp Ser
165 170 175
Gly Val Asp Asp Asp Met Ala Cys His Lys Ile Pro Val Glu Ala Asp
180 185 190
Phe Leu Tyr Ala Tyr Ser Thr Ala Pro Gly Tyr Tyr Ser Trp Arg Asn
195 200 205
Ser Lys Asp Gly Ser Trp Phe Ile Gln Ser Leu Cys Ala Met Leu Lys
210 215 220
Gln Tyr Ala Asp Lys Leu Glu Phe Met His Ile Leu Thr Arg Val Asn
225 230 235 240
Arg Lys Val Ala Thr Glu Phe Glu Ser Phe Ser Phe Asp Ala Thr Phe
245 250 255
His Ala Lys Lys Gln Ile Pro Cys Ile Val Ser Met Leu Thr Lys Glu
260 265 270
Leu Tyr Phe Tyr His
275

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GATCGGATCC ATGCGTGCGG GGACACGGGT C

31

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTACTCTAGA TCATTCACCC TGGTGGAGGA T

31

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GATCGGATCC ATGGAGAACA CTGAAAAC TC A

31

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTACTCTAGA TTAGTGATAA AAATAGAGTT C

31

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GACTATGCGT GCGGGGACAC GG

22

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AATCAAGCGT AGTCTGGGAC GTCGTATGGG TATTCACCCT GGTGGAGGAT TTG

53

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ACCATGGAGA AACTGAAAA C

21

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

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53

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